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151 AGCCTGCCTCTGCAGAAAAAAAGAACAAAAAGAAGAAAGGGAAAAGGCCCC	
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251 AAACGGCTCGTCTCTTTTAAGATCTACAACGAGGCGAAGAAAGTGAACT	
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301 GGTTTGACCAGCACCAGGGGGGGGGTGTACCTCCGCTACTCCATCCGCGCG	
L L O N D T L V O V K G L G A N G	116
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451 CTGTAAAGCCGAGAAAGACTGCGAAAACCGACCAAAAAGCCAGCC	
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A A R R R R V D O V R R II II 2 -	100
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551 CCCAGAGAAAACCTCCAAACCCAAGAAAGCGGATAAAAGTCCAGCCGTCT	100
SAKKASKPKKAKQTKKT	199
601 CTGCCAAGAAGGCGAGCAAGCCCAAGAAAGCTAAACAGACAAAAAAAGACT	000
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